

Genomic map of E. coli

E. coli

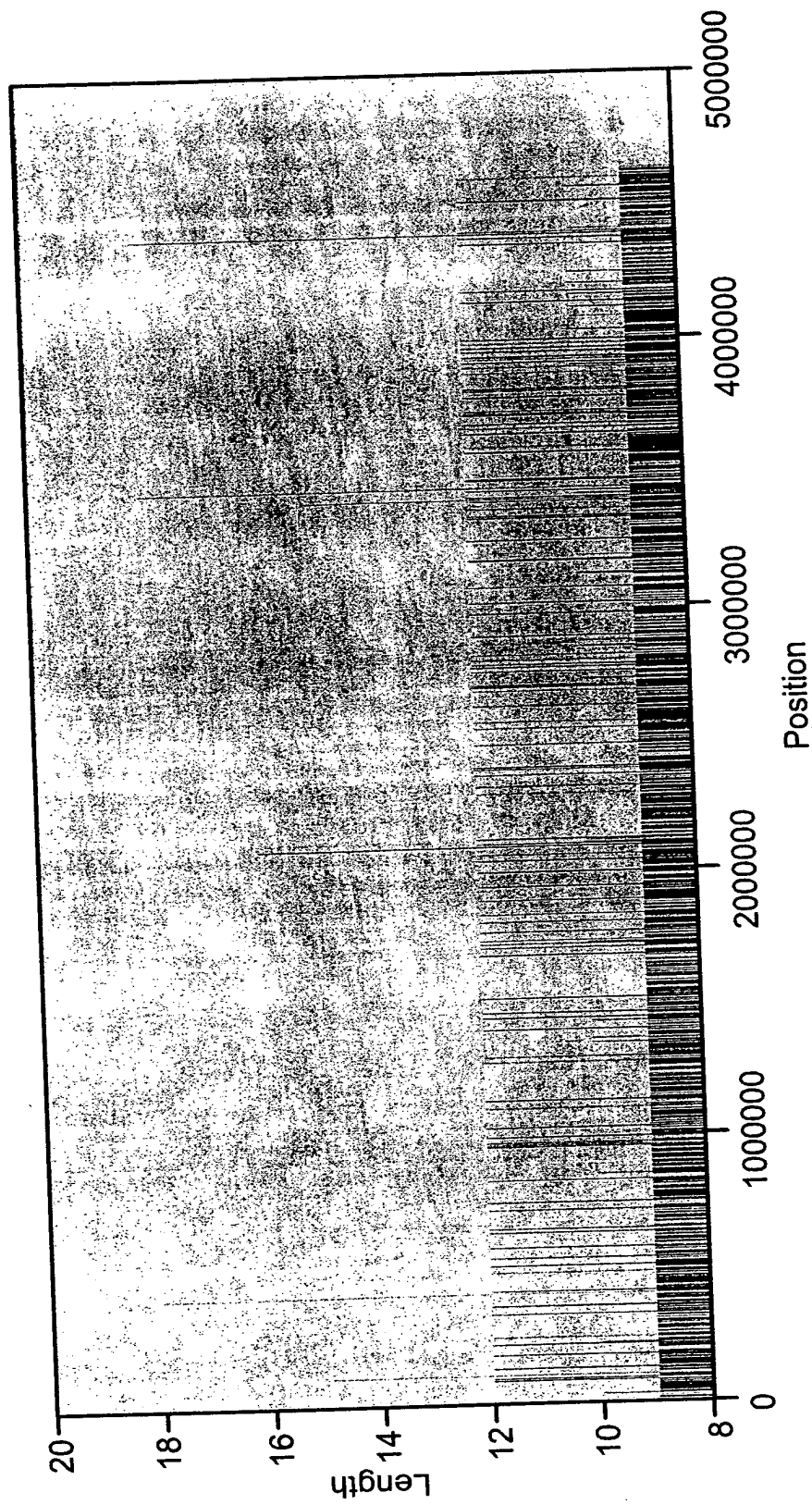


Fig. 1a

1000000 900000 800000 700000 600000 500000 400000 300000 200000 100000 0

# Bacillus Subtilis

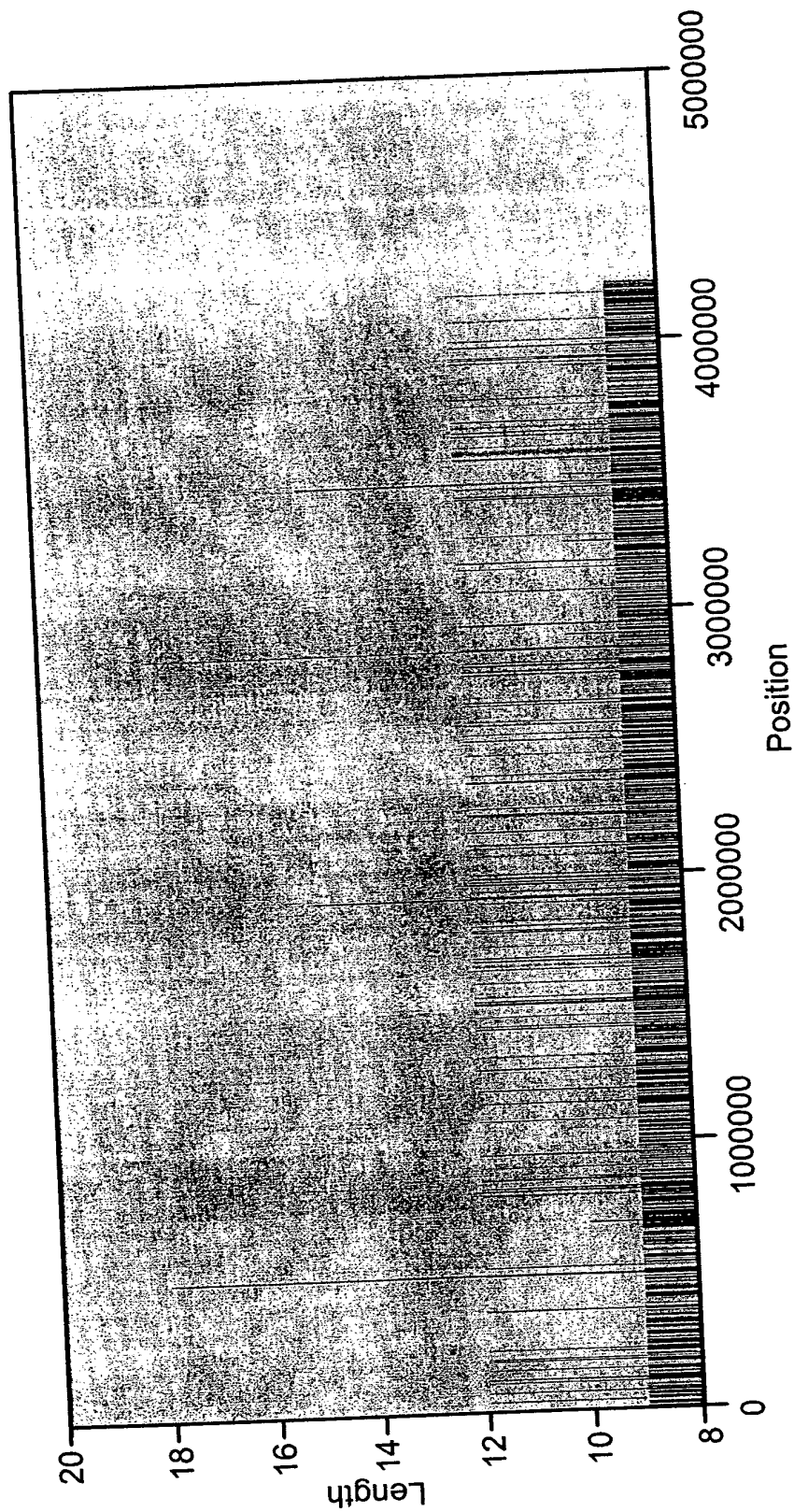


Fig. 1b

Archaeoglobus fulgidus

Archaeoglobus fulgidus

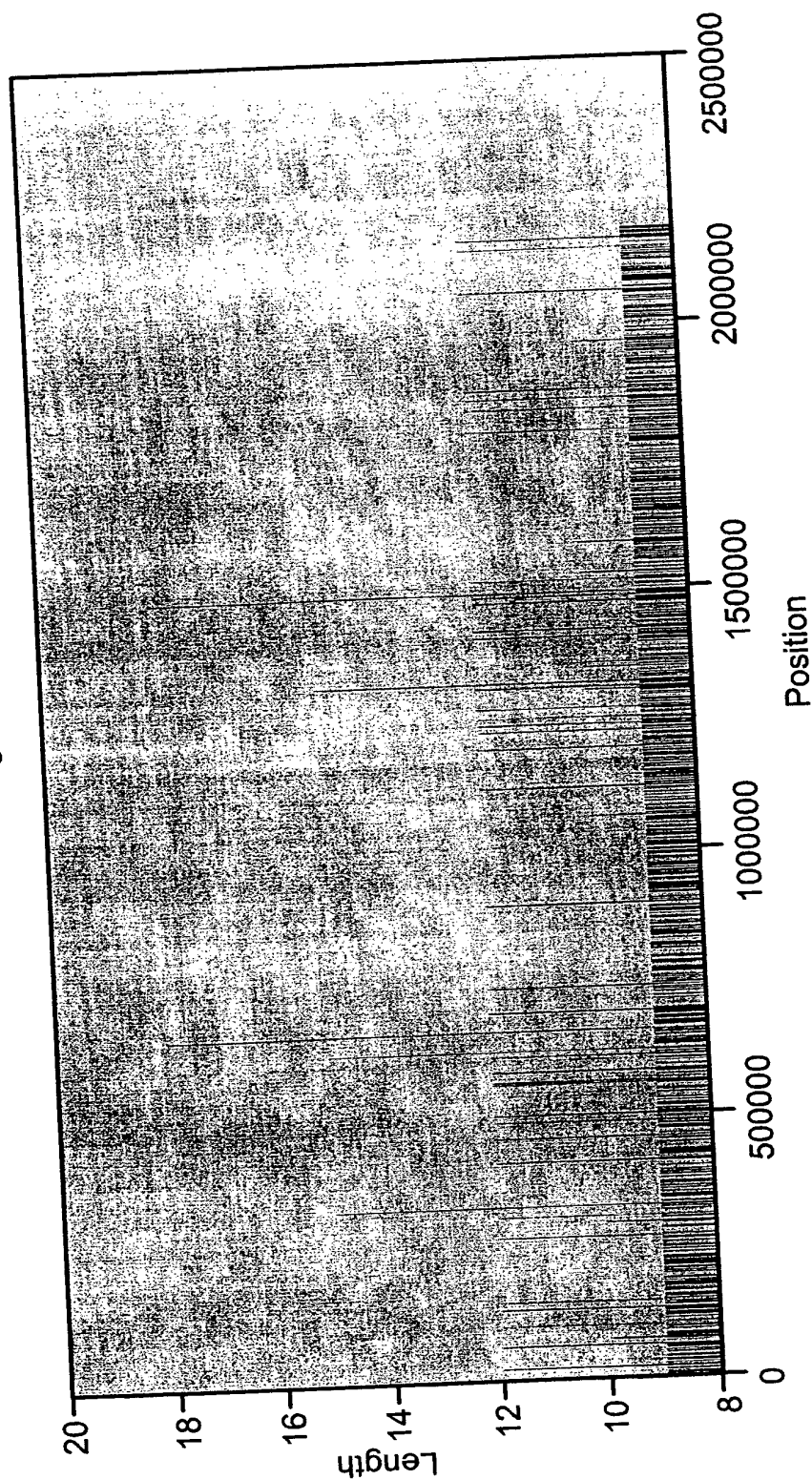
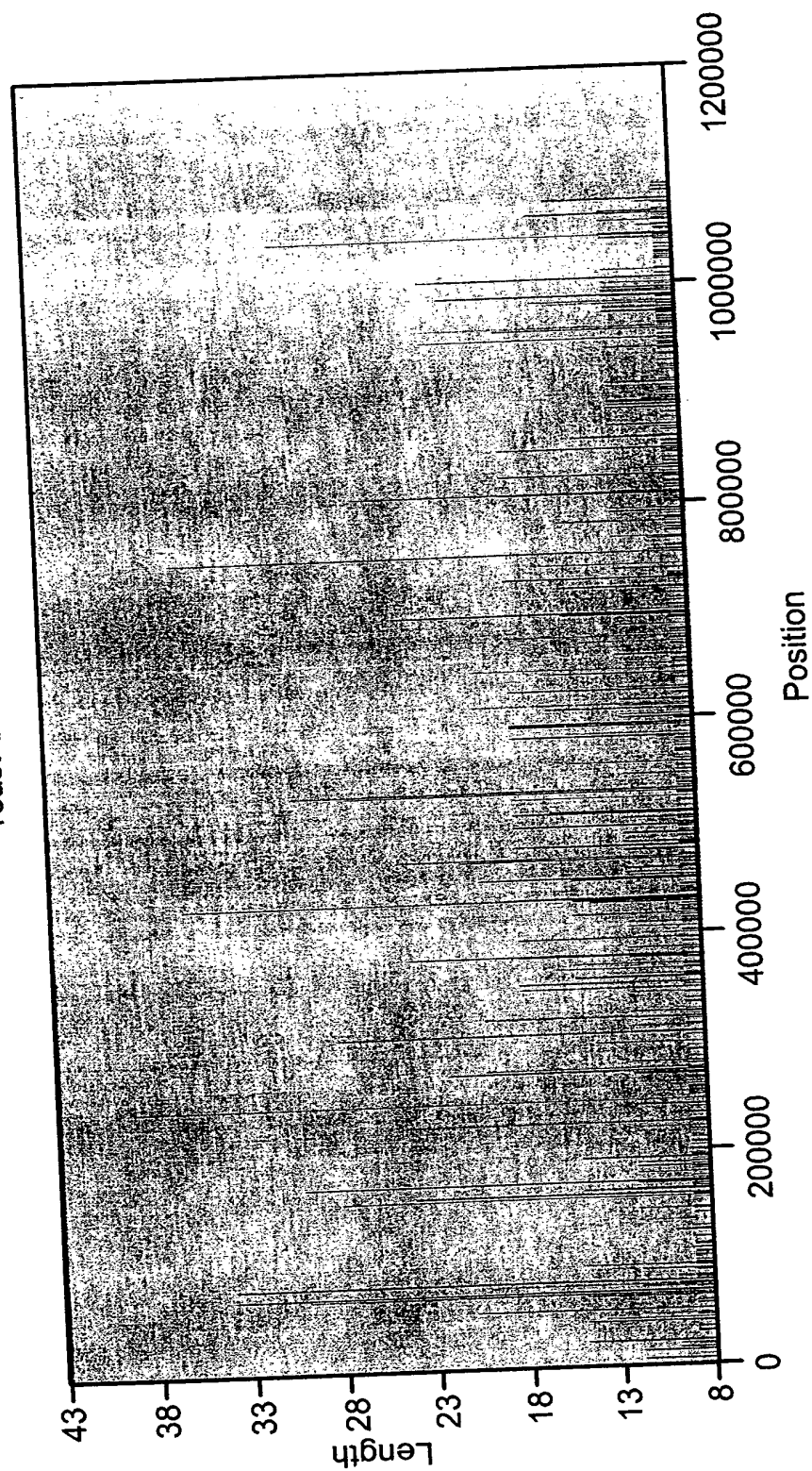
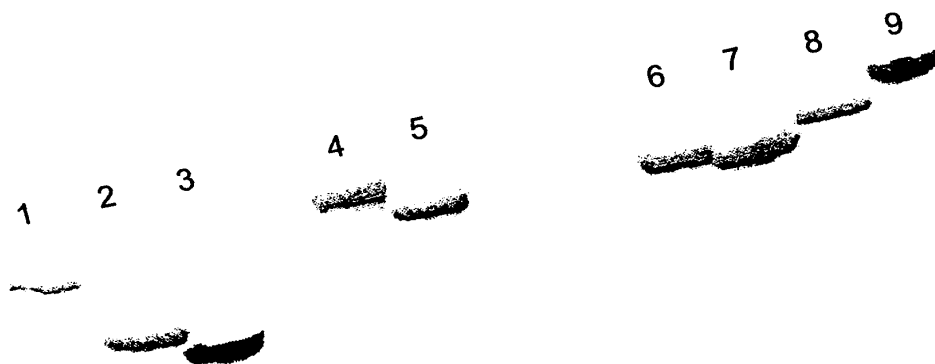


Fig. 1c

Yeast Chromosome 7

Fig. 1d



[illegible]

Ec K12, DH5α  
 Ec Bsr9b  
 Ec Bsr9c  
 Ec ETEC

Consensus

Ec K12, DH5α  
 Ec Bsr9b  
 Ec Bsr9c  
 Ec ETEC

Consensus

Ec K12, DH5α  
 Ec Bsr9b  
 Ec Bsr9c  
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Consensus

Ec K12, DH5α  
 Ec Bsr9b  
 Ec Bsr9c  
 Ec ETEC

Consensus

Ec K12, DH5α  
 Ec Bsr9b  
 Ec Bsr9c  
 Ec ETEC

Consensus

Ec K12 DH5α  
 Ec Bsr9b  
 Ec Bsr9c  
 Ec ETEC

Consensus

\* SEQ ID NO

Fig. 3a

	1				50
<i>Ec</i> K12, DH5α	TTTNCCC	GGA	AAAAA	ATAGG	AAAGGGGGG GGGCTAATCG GCAGGGAAGG 30*
<i>Ec</i> K12, w3110	TNTTN	NNCGG	AAAAA	AATNG	AAAGGGGGG GGGCTAATCG GCAGGGAAGG 31*
<i>Ec</i> Bsr9c	--TTTN	CCCG	AAAAA	AATNG	AAA..GGGGG GGGCTAATCG GCAGGGAAGG 32*
<i>Ec</i> (wt) 1	--TNTN	CCGGA	AAAAA	ANAGG	AAAGGGGGG GGGCTAATCG GCAGGGAAGG 33*
<i>Ec</i> (wt) 54	-----	NCG	GAAAA	AATG	AAA.GGGGGG GGGCTAATCG GCAGGGAAGG 34*
<i>Ec</i> (wt) 68	-----	-CG	GAAAA	AATG	AAA.GGGGGG GGGCTAATCG GCAGGGAAGG 35*

Consensus ----- -AAAAA--G AAA--GGGGG GGGCTAATCG GCAGGGAAGG 36\*

	51				100
<i>Ec</i> K12, DH5α	CCGCCCC	GGA	TAGCG	GGCGG	CANAAGGAAT CANAATTTCC AGGTCAGACG
<i>Ec</i> K12, w3110	CCGCCCC	GGA	TAGCG	GGCGG	CAGAAGGAAT CAGAATTTCC AGGTCAGACG
<i>Ec</i> Bsr9c	CCGCCCC	GGA	TAGCG	GGCGG	CAGAAGGAAT CAGAATTTCC AGGTCAGATG
<i>Ec</i> (wt) 1	CCGCCCC	GGA	TAGCG	GGCGG	CAGAAGGAAT CAGAATTTCC AGGTCAGACG
<i>Ec</i> (wt) 54	CCGCCCC	GGA	TAGCG	GGCGG	CAGAAGGAAT CAGAATTTCC AGGTCAGATG
<i>Ec</i> (wt) 68	CCGCCCC	GGA	TAGCG	GGCGG	CAGAAGGAAT CAGAATTTCC AGGTCAGATG

Consensus CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGA-G

	101				150
<i>Ec</i> K12, DH5α	GGCTG	CAAGT	TGCAG	ACCGT	TAAAATCATC GGNNGGGGTG TCGTACCACA
<i>Ec</i> K12, w3110	GGCTG	CAAGT	TGCAG	ACCGT	TAAAATCATC GGTTGGGGTG TCGTACCACA
<i>Ec</i> Bsr9c	GGCTG	CAAGT	TGCAG	ACCGT	TATAATCATC GGTTGGGGTG TCGTACCACA
<i>Ec</i> (wt) 1	GGCTG	CAAGT	TGCAG	ACCGT	TAAAATCATC GGTTGGGGTG TCGTACCACA
<i>Ec</i> (wt) 54	GGCTG	CAAGT	TGCAG	ACCGT	TATAATCATC GGTTGGGGTG TCGTACCACA
<i>Ec</i> (wt) 68	GGCTG	CAAGT	TGCAG	ACCGT	TATAATCATC GGTTGGGGTG TCGTACCACA

Consensus GGCTGCAAGT TGCAGACCGT TA-AATCATC GGTTGGGGTG TCGTACCACA

	151			180
<i>Ec</i> K12, DH5α	CTTTAC	CTGC	CAGCCC	AGATTAA-GTT -G
<i>Ec</i> K12, w3110	CTTTAC	CTGC	CAGCCC	AGATTAA-GTT -G
<i>Ec</i> Bsr9c	CTTTAC	CTGC	CAGCCC	AGATTAA-GTT -G
<i>Ec</i> (wt) 1	CTTTAC	CTGC	CAGCCC	AGATTAAAGTT TGG
<i>Ec</i> (wt) 54	CTTTAC	CTGC	CAGCCC	AGAT-AAAGTT TGG
<i>Ec</i> (wt) 68	CTTTAC	CTGC	CAGCCC	AGAT-AAAGTT TGG

Consensus CTTTACCTGC CGTCAGCCC AGAT-AA-GTT -G

\* SEQ ID NO

Fig. 3b

10

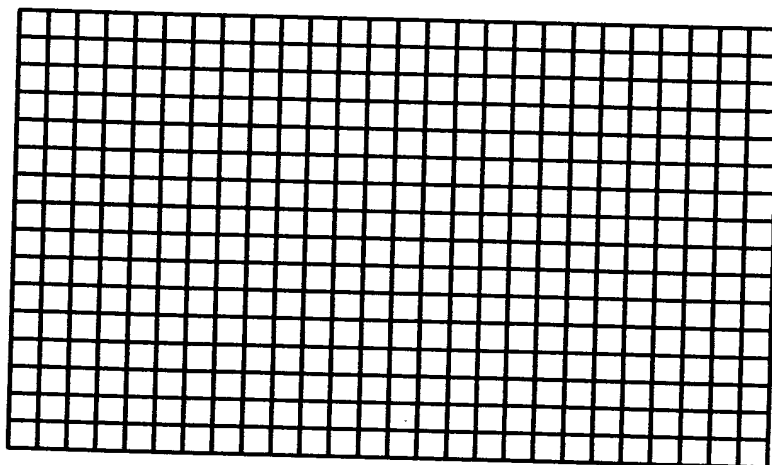


Fig. 4